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Review Article

Aeromonas veronii an emerging pathogen: A brief review

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Abstract

Aeromonas veronii, a Gram-negative bacterium, thrives in aquatic environments and is linked to diseases in animals and humans. The primary aim of this review was to provide an extensive description of *A. veronii* as an infectious agent, focusing on its microbiological attributes, pathogenesis, distribution, virulence, and antimicrobial resistance. An exhaustive review of the available medical literature was conducted. Theoretical sources were scrutinized to determine the taxonomic and microbiological properties of *A. veronii*. The pathogenic characteristics of the bacterium were examined, with a special emphasis on virulence factors, epidemiology, zoonotic potential, and antimicrobial resistance. Additionally, pertinent data regarding the geographic distribution of *A. veronii* from various origins, encompassing the environment, farm animals, and clinical cases in humans, were synthesized. This investigation illuminated the significant microbiological traits of *A. veronii*, including its adaptability to various environmental conditions and its ability to persist in crucial sources of infection, such as poultry feces and processing water. In addition, specific *A. veronii* strains, along with other *Aeromonas* species, have been identified as emerging pathogens in foodborne disease outbreaks in developing nations, accentuating the importance of rigorous hygiene measures in food production and handling. The study underscored the opportunistic nature of *A. veronii* in immunocompromised individuals, emphasizing the necessity for active surveillance and stringent hygiene practices to mitigate exposure and transmission among vulnerable populations. Furthermore, the relevance of the virulence factors of *A. veronii*, including biofilm formation and the presence of antimicrobial resistance genes, was emphasized, underscoring the importance of ongoing research to understand and combat antimicrobial resistance in this bacterium.

Keywords: *Aeromonas veronii*, pneumonia, emerging infection, emerging pathogen, aquatic bacteria

Introduction

The first case of *Aeromonas veronii* as an infectious agent causing pneumonia was reported in Ecuador (Farfán-Cano et al. 2023). Although the bacterial pathogens traditionally associated with pneumonia are *Streptococcus pneumoniae*, *Haemophilus influenzae*, and *Klebsiella pneumoniae*, which have been the subject of extensive research and medical attention, less common pathogens can also cause the disease either primarily, co-infection or opportunistic infection (Farfán-Cano et al. 2023, Parra-Vera et al. 2023, Eshwara et al. 2020). One of these emerging pathogens is *A. veronii*, a Gram-negative bacterium commonly found in aquatic environments that is occasionally implicated in human infections (Erickson et al. 2023, Liu et al. 2022, Qu at al. 2022, Sheng et al. 2021, Prediger et al. 2020, Sun et al. 2021, El-Ghany 2023). Despite its low association with pneumonia, the accurate detection and proper management of this infection are crucial to avoid misdiagnosis and ensure optimal patient care (Yee-Huang et al. 2017, Wu et al. 2019, Li et al. 2023, Xia et al. 2023, Altorre-Fernández et al. 2023, Chen et al. 2021).

A. veronii commonly found in aquatic environments and is recognised as an emerging pathogen in humans (Erickson et al. 2023, Liu et al. 2022, Qu at al. 2022, Sheng et al. 2021, Prediger et al. 2020, Sun et al. 2021). Although it mainly associated with gastroenteritis and wound infections, cases of pneumonia caused by

A. veronii are rare and often misdiagnosed because of their similarity to other bacterial infections or limited microbiological means of identification (Yee-Huang et al. 2017, Wu et al. 2019, Li et al. 2023, Xia et al. 2023, Altorre-Fernández et al. 2023).

The emergence of rare pathogens causing pneumonia is a critical public health concern. *A. veronii*, primarily associated with aquatic environments, poses a unique challenge due to its rare occurrence in lung infections. This systematic review is a valuable contribution to the medical community by providing information on the clinical presentation, diagnostic approaches, and treatment modalities for pneumonia caused by *A. veronii*. An improved understanding of these cases may lead to greater diagnostic accuracy, optimized therapeutics, and improved patient outcomes.

Methods

A systematic search for information on *A. veronii* as an infectious agent was performed in PubMed as of 9 August 2023. An analysis synthesis and review of relevant literature related to infections associated with *A. veronii* were carried out. The literature search was conducted using PubMed, applying filters including "free full text" case reports, and "humans". The choice of this database was based on its broad coverage of scientific literature as well as its focus on the medical and health fields. Diagnostic approaches, including microbiological culture and molecular identification methods, were evaluated in terms of their accuracy and limitations. Treatment protocols, including antibiotic selection and patient response, were discussed in relation to existing guidelines and the susceptibility profiles of the bacteria.

A search strategy was designed to identify relevant articles related to *A. veronii* pneumonia. The search terms used were "*Aeromonas veronii*" and "pneumonia". Filters were used to ensure the inclusion of human studies and articles available in English and Spanish. In addition, the search was limited to the last five years to ensure the inclusion of recent research.

Microbiological aspects

A. veronii is part of the genus *Aeromonas*, belonging to the family Aeromonadaceae, and is characterized as a group of facultatively aerobic Gram-negative bacteria that are widely distributed in aquatic environments and have also been associated with diseases in animals and humans (Erickson et al. 2023). *Aeromonas* has a wide geographical distribution and can cause various diseases in humans. It is common in cold-blooded animals such as fish (Sun et al. 2021), and is attributed to aeromoniasis, a global clinical disease of poultry that has been detected in various parts of the world, causing localized or systemic infections, alone or in combination with other infections (El-Ghany 2023). *Aeromonas* can adapt to diverse ecological sites on their hosts and have striking characteristics that allow them to survive under a variety of environmental conditions (Xia et al. 2023). Live poultry faeces, carcasses, and processing water in poultry plants are important sources of infection (Sun et al. 2021).

Aeromonas is Gram-negative, non-spore-forming, rod-shaped, facultative anaerobic, and positive for oxidase, catalase, and indole (El-Ghany 2023). The genus *Aeromonas* comprises more than 36 species, including *A. hydrophila, A. caviae, A. media*, and *A. veronii* biovar. sobria, and *A. veronii* biovar. veronii is of particular clinical importance (Sun et al. 2021, Zhou et al. 2019).

Aeromonas has been associated with foodborne disease outbreaks, particularly in developing countries that face hygiene challenges (Sun et al. 2021, Zhou et al. 2019). Certain strains, such as *A. hydrophila, A. sobria,* and *A. caviae*, have been linked to emerging pathogens that cause gastroenteritis and extraintestinal diseases in humans (Erickson et al. 2023, Zhou et al. 2019). There is little information on aeromoniasis



in poultry, as most research focuses on the infection of aquatic animals and the presence of Aeromonas spp. in poultry products (El-Ghany 2023).

Geographical distribution and virulence

A. veronii has been isolated from various sources including the environment (air, water, and soil), food animals, and clinical infections in humans (Chen et al. 2021). The hospital environment is an essential reservoir of microorganisms capable of causing infections, and there are often no specific recommendations to prevent, control, or monitor the presence of these pathogens, as in the case of the genus *Aeromonas*, which is considered an emerging pathogen as it is isolated from drinking water systems, food, detergents, and patients in hospitals and presents multiple virulence factors associated with the development of infections (Alatorre-Fernández et al. 2023).

Virulence factors include aerolysin, enterotoxins, hemolysin, protease, hemagglutinins, endotoxin, siderophores, Shiga-like toxin, type II, III, IV, and VI secretion systems (TISS), polar and lateral flagella, pili, and the ability to form biofilm (Alatorre-Fernández et al. 2023). The pathology and virulence of *Aeromonas* spp. result from stress responses and heat shock proteins. Intestinal and systemic infections are mediated by numerous virulence factors, including endotoxins, cytotoxic enterotoxins, cytotoxins, hemolysins, adhesins, and extracellular enzymes such as proteases, amylases, lipases, ADP-ribosyltransferases and DNases (Prediger et al. 2020, Zhou et al. 2019). The expression of virulence factors in *Aeromonas* is linked to gene regulatory cascades associated with interactions between pathogens and the environment (Zhou et al. 2019, Zhang et al. 2019).

Different *Aeromonas* species harbor virulence genes such as hemolysin (*hlyA*), aerolysin (*aerA*), and extracellular deoxyribonuclease (*exu*), each of which plays an essential role in pathogenicity related to diarrheal diseases; for example, the *exu* gene encodes an extracellular DNase that blocks host antibacterial defences (Liu et al. 2022). Their presence correlates with the ability of bacteria to invade, colonize, and survive in the host immune system. In addition, many toxin genes have been identified in *Aeromonas spp.* (Liu et al. 2022, Yee-Huang et al. 2017, Fernández-Bravo et al. 2022, Qu et al. 2022).

Biofilm formation is another vital virulence factor that plays a role in bacterial adhesion and colonisation on the host's intestinal epithelial surface and villi, as well as in reducing antibiotic susceptibility and recognition by the immune system; biofilm-forming *Aeromonas* isolates have already been reported in poultry and poultry workers (El-Ghany 2023, Alatorre-Fernández et al. 2023, Yang et al. 2022).

Human opportunism

Opportunism of *A. veronii* in humans refers to its ability to cause infections in individuals with compromised or weakened immune systems (Farfán-Cano et al. 2023, Parra-Vera et al. 2023). Although Aeromonas is commonly a part of the normal microbiome in aquatic environments and in some animals, it can become pathogenic under certain circumstances (Chen et al. 2021).

In individuals with a healthy immune system, exposure to *A. veronii* generally does not result in a serious illness. However, in people with immunodeficiency or medical conditions that weaken the body's defences, such as people with chronic diseases, transplant recipients, cancer patients or people with HIV/AIDS, *A. veronii* may take the opportunity to cause infections (Liu et al. 2022, Li et al. 2023, Alatorre-Fernández et al. 2023, Chen et al. 2021).

Opportunistic *A. veronii* infections in humans can manifest in various ways, including gastroenteritis, wound infections, sepsis, pneumonia, and other extraintestinal

infections. These infections range in severity from mild, self-limiting symptoms to more severe cases that require medical treatment and antimicrobials (Yee-Huang et al. 2017, Wu et al. 2019, Li et al. 2023, Xia et al. 2023, Altorre-Fernández et al. 2023). The opportunism of *A. veronii* in humans underlines the importance of active and careful surveillance in vulnerable populations as well as hygiene and proper handling of food and water to prevent the exposure and spread of these bacteria (Yee-Huang et al. 2017, Wu et al. 2019, Li et al. 2023, Altorre-Fernández et al. 2023).

Pathogenicity

The pathogenicity of *Aeromonas spp*. involves multiple virulence factors, and is especially prominent in *A. veronii*, which causes local and systemic infections in several species, including poultry. In this context, *A. hydrophila*, a species of the same genus, has been found to trigger infections in poultry, sometimes in conjunction with other pathogens such as Salmonellae and the agent of fowl cholera (Qu et al. 2022, Prediger et al. 2020, Sun et al. 2021).

A. hydrophila infections in poultry, such as the Japanese quail, result in symptoms such as depression, ruffled plumage, severe diarrhea, and liver congestion. In experiments, inoculation with *A. hydrophila* in one- and five-day-old chickens led to high mortality (60–100%), gastrointestinal disorders, and congestion in multiple organs, including the liver, spleen, lungs, kidneys, and intestine. Liver hemorrhage, omphalitis, enteritis, and nephrosis have also been observed. In addition, the virulence of *A. hydrophila* has been found to vary according to the dose of infection, with subcutaneous injections at different concentrations resulting in significant differences in mortality rate and severity of symptoms (Qu et al. 2022, Prediger et al. 2020, El-Ghany 2023, Zhang et al. 2019).

Antimicrobial resistance

In a study, *A. veronii* strains carrying the blaKPC-24 carbapenem resistance gene were identified (Yang et al. 2022). These strains showed variability in their susceptibility to ceftazidime compared with those harboring the *blaKPC-2* gene. These differences could originate from mutations in the KPC enzymes or signal peptide sequences (Yang et al. 2022). Resistance to carbapenemics, as in blaKPC-24 strains, is often due to carbapenemases, enzymes that hydrolyze these broad-spectrum antibiotics. The blaKPC-24 gene identified in this study encodes these enzymes (Yang et al. 2022). Resistance gene transfer occurs via conjugation, transduction, and transformation. In conjugation, bacterial cells transfer genes directly, transduction carries them via bacteriophages, and transformation involves direct acquisition of environmental DNA (Yang et al. 2022).

Plasmids are mobile genetic elements that can carry resistance genes between different bacteria, allowing them to acquire antibiotic resistance quickly and efficiently through horizontal gene transfer. In the case of *A. veronii* and other bacterial pathogens, plasmids can be an important vehicle for the acquisition of antibiotic resistance genes, including carbapenems (Sheng et al. 2021, Prediger et al. 2020, Sun et al. 2021, Zhou et al. 2019, Yang et al. 2022, Montes et al. 2023).

A. veronii has the ability to acquire resistance through the transfer of resistance genes on plasmids, as well as through mutations in its own genes. In the case of strains carrying the *blaKPC-24* gene, resistance is mediated by the production of the enzyme carbapenemase KPC-24, whereas other strains can develop resistance through mechanisms such as efflux pumps (Shent et al. 2021, Yang et al. 2022, Montes et al. 2023).

Conclusions

The present study provides a brief review of the taxonomic and microbiological characteristics of *A. veronii*. The bacterium can cause localized or systemic infections, often in combination with other pathogens, and that poultry feces and processing water are significant sources of infection. The virulence factors of *A. veronii*, including various toxins, secretion systems, flagella, pili, and biofilm formation. These factors contribute to the ability of the bacterium to colonize and cause infections in hosts. Specific virulence genes, such as hemolysin, aerolysin, and extracellular deoxyribonuclease, are highlighted.

A. veronii is opportunistic in humans, causing infections mainly in individuals with compromised immune systems. It outlines the types of infections that can occur, ranging from mild gastroenteritis to more severe cases requiring medical treatment. The text emphasizes the need for surveillance, hygiene, and proper food and water handling to prevent exposure and spread.

Authors' contributions

Conceptualization: PHJ; Data Curation: PHJ, FGG and BDC; Formal Analysis: PHJ; Investigation: PHJ, FGG and BDC; Methodology: PHJ, FGG and BDC; Validation: PHJ, FGG and BDC; Writing – Original Draft Preparation: PHJ, FGG and BDC; Writing – Review & Editing: PHJ, FGG and BDC.

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Conflict of interest

There are no competing interests that exist.

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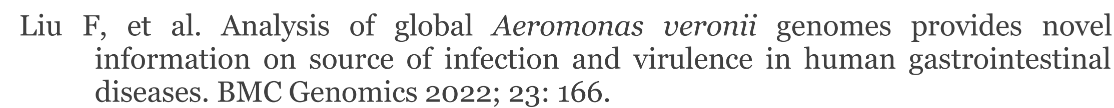
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